

4-32761A_UNZ.ST25.txt
SEQUENCE LISTING

<110> Novartis AG

<120> Organic Compound

<130> 4-32761P1/UNZ

<160> 44

<170> PatentIn version 3.1

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<213> Rattus norvegicus

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<221> PEPTIDE

<222> (1)..(18)

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<213> Mus musculus

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<223> Variable part of Heavy Chain of 11C7 with leader sequence

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Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
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Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro
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Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
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Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr
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Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln
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Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
130 135 140

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
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Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
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Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
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50 55 60

Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
65 70 75 80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys
100 105 110

Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu
115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
130 135 140

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Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
 145 150 155 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
 165 170 175

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 180 185 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
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gac gag gag gaa gaa gag gag gag gaa gag gag gac gag gac gaa gac		144
Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp		
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ctg gag gag ctg gag gtg ctg gag agg aag ccc gcc gcc ggg ctg tcc		192
Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser		
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gcg gcc cca gtg ccc acc gcc cct gcc gcc ggc gcg ccc ctg atg gac		240

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gct	ccc	ccc	gtc	gcc	ccg	gag	cg	cg	ccg	tct	tgg	gac	ccg	agc	ccg	336
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cct	gct	gca	tct	gag	cct	gtg	ata	cgc	tcc	tct	gca	gaa	aat	atg	gac	624
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Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro	Ser	Leu	Ser	Pro	
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Leu	Thr	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	Gly	Ser	Ser	Phe	
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340 345 350	
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Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser	
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Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr	
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Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala	
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Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu	
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785 790 795 800	
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Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu	
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Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro	
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acc	tat	gtt	ggt	gcc	ttg	ttt	aat	ggt	ctg	aca	cta	ctg	att	ttg	3429
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1160						1165					1170				
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1190															

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35 40 45

Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
50 55 60

Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
65 70 75 80

Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95

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100 105 110

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165 170 175

Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu
180 185 190

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195 200 205

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210 215 220

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225 230 235 240

Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser
245 250 255

Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala
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Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr
370 375 380

Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys
385 390 395 400

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405 410 415

Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr
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Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro
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Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys
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Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro
580 585 590

Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser
595 600 605

Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val
610 615 620

Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu
625 630 635 640

Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro
645 650 655

Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly
660 665 670

Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln
675 680 685

Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu
690 695 700

Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu
705 710 715 720

Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu
725 730 735

Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser
740 745 750

Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys
755 760 765

Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn
770 775 780

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Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu
785 790 795 800

Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro
805 810 815

Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met
820 825 830

Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser
835 840 845

Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro
850 855 860

Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp
865 870 875 880

Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His
885 890 895

Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys
900 905 910

Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val
915 920 925

Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala
930 935 940

Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr
945 950 955 960

Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu
965 970 975

Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro
980 985 990

Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu
995 1000 1005

Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala
1010 1015 1020

Ser Leu Phe Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser
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1025 1030 1035

Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser
1040 1045 1050

Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp
1055 1060 1065

Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile
1070 1075 1080

Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His
1085 1090 1095

Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp
1100 1105 1110

Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe
1115 1120 1125

Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu
1130 1135 1140

Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His
1145 1150 1155

Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val
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Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys
1175 1180 1185

Arg Lys Ala Glu
1190

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<212> PRT
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<220>
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<223> Human NogoA_623-640

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Glu Ala

<210> 7

<211> 819

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(819)

<223> human Nig

<400> 7

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35 40 45Ser Leu Pro Ser Leu Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His
50 55 60Glu Tyr Leu Gly Asn Leu Ser Thr Val Leu Pro Thr Glu Gly Thr Leu
65 70 75 80Gln Glu Asn Val Ser Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys
85 90 95Thr Leu Leu Ile Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr
100 105 110

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Ser Glu Met Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala
115 120 125

Val Ile Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp
130 135 140

Glu Glu Glu Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu
145 150 155 160

Leu Pro Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser
165 170 175

Ser Glu Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu
180 185 190

Ala Pro Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val
195 200 205

Trp Glu Val Lys Asp Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly
210 215 220

Gly Lys Ile Glu Ser Asn Leu Glu Ser Lys Val Asp Lys Lys Cys Phe
225 230 235 240

Ala Asp Ser Leu Glu Gln Thr Asn His Glu Lys Asp Ser Glu Ser Ser
245 250 255

Asn Asp Asp Thr Ser Phe Pro Ser Thr Pro Glu Gly Ile Lys Asp Arg
260 265 270

Ser Gly Ala Tyr Ile Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu
275 280 285

Ser Ile Ala Thr Asn Ile Phe Pro Leu Leu Gly Asp Pro Thr Ser Glu
290 295 300

Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Lys Lys Ala Gln Ile Val
305 310 315 320

Thr Glu Lys Asn Thr Ser Thr Lys Thr Ser Asn Pro Phe Leu Val Ala
325 330 335

Ala Gln Asp Ser Glu Thr Asp Tyr Val Thr Thr Asp Asn Leu Thr Lys
340 345 350

Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp
355 360 365

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Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr
370 375 380

Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val
385 390 395 400

Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu
405 410 415

Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu
420 425 430

Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln
435 440 445

Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile
450 455 460

Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val
465 470 475 480

Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu
485 490 495

Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile
500 505 510

Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro
515 520 525

Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro Val Pro
530 535 540

Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu Pro Val
545 550 555 560

Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp
565 570 575

Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu
580 585 590

Ser Met Ile Glu Tyr Glu Asn Lys Glu Lys Leu Ser Ala Leu Pro Pro
595 600 605

Glu Gly Gly Lys Pro Tyr Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn

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Thr Lys Asp Thr Leu Leu Pro Asp Glu Val Ser Thr Leu Ser Lys Lys
 625 630 635 640

Glu Lys Ile Pro Leu Gln Met Glu Glu Leu Ser Thr Ala Val Tyr Ser
 645 650 655

Asn Asp Asp Leu Phe Ile Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu
 660 665 670

Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr
 675 680 685

Leu Ile Ser Ser Lys Thr Asp Ser Phe Ser Lys Leu Ala Arg Glu Tyr
 690 695 700

Thr Asp Leu Glu Val Ser His Lys Ser Glu Ile Ala Asn Ala Pro Asp
 705 710 715 720

Gly Ala Gly Ser Leu Pro Cys Thr Glu Leu Pro His Asp Leu Ser Leu
 725 730 735

Lys Asn Ile Gln Pro Lys Val Glu Glu Lys Ile Ser Phe Ser Asp Asp
 740 745 750

Phe Ser Lys Asn Gly Ser Ala Thr Ser Lys Val Leu Leu Leu Pro Pro
 755 760 765

Asp Val Ser Ala Leu Ala Thr Gln Ala Glu Ile Glu Ser Ile Val Lys
 770 775 780

Pro Lys Val Leu Val Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr
 785 790 795 800

Glu Lys Glu Asp Arg Ser Pro Ser Ala Ile Phe Ser Ala Glu Leu Ser
 805 810 815

Lys Thr Ser

<210> 8
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<212> PRT
<213> Mus musculus

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<220>
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<210> 9

<211> 17

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Asp

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<211> 9

<212> PRT

<213> *Mus musculus*

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4-32761A_UNZ.ST25.txt

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<211> 16

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Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Tyr Leu Asn
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<210> 12

<211> 7

<212> PRT

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<223> hypervariable part of light chain of 11C7

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Leu Val Ser Lys Leu Asp Ser
1 5

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<210> 13
<211> 9
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<213> *Mus musculus*

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<223> hypervariable part of light chain of 11C7

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1 5

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<212> DNA
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<220>
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30

<210> 15
<211> 51
<212> DNA
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<220>
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<222> (1)..(51)

<223> DNA-CDR2-11C7

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51

<210> 16

<211> 27

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<213> Mus musculus

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<221> misc_binding

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<223> DNA-CDR3-11C7

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27

<210> 17

<211> 48

<212> DNA

<213> Mus musculus

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<222> (1)..(48)

<223> DNA-CDR'1-11C7

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aagtcaagtc agagcctctt gcatagtgat ggaaagacat atttgaat

48

<210> 18

<211> 21

4-32761A_UNZ.ST25.txt

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1)..(21)

<223> DNA-CDR'2-11C7

<400> 18

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21

<210> 19

<211> 27

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<221> misc_binding

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<223> DNA-CDR'3-11C7

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<210> 20

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<221> CDS

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<223> Leader sequence for heavy chain of 11C7

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Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
1 5 10 15

cag tgt 54
Gln Cys

<210> 21

<211> 18

<212> PRT

<213> Mus musculus

<400> 21

Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val 15
1 5 10 15

Gln Cys

<210> 22

<211> 57

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(57)

<223> leader sequence for 11C7-light chain

<400> 22
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1 5 10 15

acc agc ggt 57
Thr Ser Gly

<210> 23

4-32761A_UNZ.ST25.txt

<211> 19

<212> PRT

<213> *Mus musculus*

<400> 23

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
1 5 10 15

Thr Ser Gly

<210> 24

<211> 181

<212> PRT

<213> *Homo sapiens*

<220>

<221> PEPTIDE

<222> (1)..(181)

<223> human Nig-D20

<400> 24

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser
1 5 10 15

Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser
20 25 30

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
35 40 45

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val
50 55 60

Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
65 70 75 80

Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
85 90 95

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Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
100 105 110

Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile
115 120 125

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro
130 135 140

Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro
145 150 155 160

Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu
165 170 175

Pro Val Asp Leu Phe
180

<210> 25

<211> 3492

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)..(3492)

<223> rat NogoA

<400> 25

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1 5 10 15

ccg ccc cgg cct ccg ccc gcc ttc aag tac cag ttc gtg acg gag ccc
Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro
20 25 30

gag gac gag gag gac gag gag gag gag gac gag gag gag gac gag
Glu Asp Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp
35 40 45

gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc gca gcc ggg
Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly
50 55 60

ctg tcc gca gct gcg gtg ccg ccc gcc gcc gac gac
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Leu	Ser	Ala	Ala	Ala	Val	Pro	Pro	Ala	Ala	Ala	Pro	Leu	Leu	Asp		
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Phe	Ser	Ser	Asp	Ser	Val	Pro	Pro	Ala	Pro	Arg	Gly	Pro	Leu	Pro	Ala	
					85				90				95			
gcg	ccc	cct	gcc	gct	cct	gag	agg	cag	cca	tcc	tgg	gaa	cgc	agc	ccc	336
Ala	Pro	Pro	Ala	Ala	Pro	Glu	Arg	Gln	Pro	Ser	Trp	Glu	Arg	Ser	Pro	
					100			105				110				
gcg	gcg	ccc	gct	cca	tcc	ctg	ccg	ccc	gct	gcc	gca	gtc	ctg	ccc	tcc	384
Ala	Ala	Pro	Ala	Pro	Ser	Leu	Pro	Pro	Ala	Ala	Ala	Val	Leu	Pro	Ser	
					115			120				125				
aag	ctc	cca	gag	gac	gac	gag	cct	ccg	gct	gct	agg	ccc	ccg	cct	ccg	432
Lys	Leu	Pro	Glu	Asp	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro	Pro	Pro	Pro	
					130			135				140				
cca	gcc	ggc	gct	agc	ccc	ctg	gct	gag	ccc	gcc	gct	ccc	cct	tcc	acg	480
Pro	Ala	Gly	Ala	Ser	Pro	Leu	Ala	Glu	Pro	Ala	Ala	Pro	Pro	Pro	Ser	
					145			150				155			160	
ccg	gcc	gct	ccc	aag	cgc	agg	ggc	tcc	ggc	tca	gtg	gat	gag	acc	ctt	528
Pro	Ala	Ala	Pro	Lys	Arg	Arg	Gly	Ser	Gly	Ser	Val	Asp	Glu	Thr	Leu	
					165			170				175				
ttt	gct	ctt	cct	gct	gca	tct	gag	cct	gtg	ata	ccc	tcc	tct	gca	gaa	576
Phe	Ala	Leu	Pro	Ala	Ala	Ser	Glu	Pro	Val	Ile	Pro	Ser	Ser	Ala	Glu	
					180			185				190				
aaa	att	atg	gat	ttg	atg	gag	cag	cca	ggt	aac	act	gtt	tgc	tct	ggt	624
Lys	Ile	Met	Asp	Leu	Met	Glu	Gln	Pro	Gly	Asn	Thr	Val	Ser	Ser	Gly	
					195			200				205				
caa	gag	gat	ttc	cca	tct	gtc	ctg	ctt	gaa	act	gct	gcc	tct	ctt	cct	672
Gln	Glu	Asp	Phe	Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro	
					210			215				220				
tct	cta	tct	ctc	tca	act	gtt	tct	ttt	aaa	gaa	cat	gga	tac	ctt		720
Ser	Leu	Ser	Pro	Leu	Ser	Thr	Val	Ser	Phe	Lys	Glu	His	Gly	Tyr	Leu	
					225			230				235			240	
ggt	aac	tta	tca	gca	gtg	tca	tcc	tca	gaa	gga	aca	att	gaa	gaa	act	768
Gly	Asn	Leu	Ser	Ala	Val	Ser	Ser	Ser	Glu	Gly	Thr	Ile	Glu	Glu	Thr	
					245			250				255				
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Leu	Asn	Glu	Ala	Ser	Lys	Glu	Leu	Pro	Glu	Arg	Ala	Thr	Asn	Pro	Phe	
					260			265				270				
gta	aat	aga	gat	tta	gca	gaa	ttt	tca	gaa	tta	gaa	tat	tca	gaa	atg	864
Val	Asn	Arg	Asp	Leu	Ala	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	
					275			280				285				
gga	tca	tct	ttt	aaa	ggc	tcc	cca	aaa	gga	gag	tca	gcc	ata	tta	gta	912
Gly	Ser	Ser	Phe	Lys	Gly	Ser	Pro	Lys	Gly	Glu	Ser	Ala	Ile	Leu	Val	
					290			295				300				
gaa	aac	act	aag	gaa	gaa	gta	att	gtg	agg	agt	aaa	gac	aaa	gag	gat	960
Glu	Asn	Thr	Lys	Glu	Glu	Val	Ile	Val	Arg	Ser	Lys	Asp	Lys	Glu	Asp	
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325 330 335	
aaa gaa gac aga gtt gtg tct cca gaa aag aca atg gac att ttt aat	1056
Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn	
340 345 350	
gaa atg cag atg tca gta gta gca cct gtg agg gaa gag tat gca gac	1104
Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp	
355 360 365	
ttt aag cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga	1152
Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly	
370 375 380	
agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg gac	1200
Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp	
385 390 395 400	
aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag gat	1248
Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp	
405 410 415	
agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc cca gaa cct	1296
Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro	
420 425 430	
gtg aag gac agc tcc aga gca tat att acc ttt gct tcc ttt acc tca	1344
Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser	
435 440 445	
gca acc gaa agc acc aca gca aac act ttc cct ttg tta gaa gat cat	1392
Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His	
450 455 460	
act tca gaa aat aaa aca gat gaa aaa aaa ata gaa gaa agg aag gcc	1440
Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala	
465 470 475 480	
caa att ata aca gag aag act agc ccc aaa acg tca aat cct ttc ctt	1488
Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu	
485 490 495	
gta gca gta cag gat tct gag gca gat tat gtt aca aca gat acc tta	1536
Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu	
500 505 510	
tca aag gtg act gag gca gca gtg tca aac atg cct gaa ggt ctg acg	1584
Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr	
515 520 525	
cca gat tta gtt cag gaa gca tgt gaa agt gaa ctg aat gaa gcc aca	1632
Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr	
530 535 540	
ggt aca aag att gct tat gaa aca aaa gtg gac ttg gtc caa aca tca	1680
Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser	
545 550 555 560	
gaa gct ata caa gaa tca ctt tac ccc aca gca cag ctt tgc cca tca	1728
Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser	
565 570 575	

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ttt gag gaa gct gaa gca act ccg tca cca gtt ttg cct gat att gtt	1776
Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val	
580 585 590	
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Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val	
595 600 605	
gtg cag ccc agt gta tcc cca ctg gaa gca cct cct cca gtt agt tat	1872
Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr	
610 615 620	
gac agt ata aag ctt gag cct gaa aac ccc cca cca tat gaa gaa gcc	1920
Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala	
625 630 635 640	
atg aat gta gca cta aaa gct ttg gga aca aag gaa gga ata aaa gag	1968
Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu	
645 650 655	
cct gaa agt ttt aat gca gct gtt cag gaa aca gaa gct cct tat ata	2016
Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile	
660 665 670	
tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc act gag cca	2064
Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro	
675 680 685	
agt cca gat ttc tct aat tat tca gaa ata gca aaa ttc gag aag tcg	2112
Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser	
690 695 700	
gtg ccc gaa cac gct gag cta gtg gag gat tcc tca cct gaa tct gaa	2160
Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu	
705 710 715 720	
cca gtt gac tta ttt agt gat gat tcg att cct gaa gtc cca caa aca	2208
Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr	
725 730 735	
caa gag gag gct gtg atg ctc atg aag gag agt ctc act gaa gtg tct	2256
Gln Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser	
740 745 750	
gag aca gta gcc cag cac aaa gag gag aga ctt agt gcc tca cct cag	2304
Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln	
755 760 765	
gag cta gga aag cca tat tta gag tct ttt cag ccc aat tta cat agt	2352
Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser	
770 775 780	
aca aaa gat gct gca tct aat gac att cca aca ttg acc aaa aag gag	2400
Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu	
785 790 795 800	
aaa att tct ttg caa atg gaa gag ttt aat act gca att tat tca aat	2448
Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn	
805 810 815	
gat gac tta ctt tct tct aag gaa gac aaa ata aaa gaa agt gaa aca	2496
Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr	

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 820 825 830

ttt tca gat tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt	Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe	2544
835 840 845	845	
gtc agt gct aaa gat gat tct cct aaa tta gcc aag gag tac act gat	Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp	2592
850 855 860	860	
cta gaa gta tcc gac aaa agt gaa att gct aat atc caa agc ggg gca	Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala	2640
865 870 875 880	880	
gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag aat	Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn	2688
885 890 895	895	
ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc gaa aat	Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn	2736
900 905 910	910	
agg tcc agt gta tct aag gca tcc ata tcg cct tca aat gtc tct gct	Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala	2784
915 920 925	925	
ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa tcc aaa tca ctt	Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu	2832
930 935 940	940	
acg aaa gaa gca gag aaa aaa ctt cct tct gac aca gag aaa gag gac	Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp	2880
945 950 955 960	960	
aga tcc ctg tca gct gta ttg tca gca gag ctg agt aaa act tca gtt	Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val	2928
965 970 975	975	
gtt gac ctc ctc tac tgg aga gac att aag aag act gga gtg gtg ttt	Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe	2976
980 985 990	990	
ggt gcc agc tta ttc ctg ctg ctg tct ctg aca gtg ttc agc att gtc	Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val	3024
995 1000 1005	1005	
agt gta acg gcc tac att gcc ttg gcc ctg ctc tcg gtg act atc	Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Ser Val Thr Ile	3069
1010 1015 1020	1020	
agc ttt agg ata tat aag ggc gtg atc cag gct atc cag aaa tca	Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser	3114
1025 1030 1035	1035	
gat gaa ggc cac cca ttc agg gca tat tta gaa tct gaa gtt gct	Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala	3159
1040 1045 1050	1050	
ata tca gag gaa ttg gtt cag aaa tac agt aat tct gct ctt ggt	Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly	3204
1055 1060 1065	1065	
cat gtg aac agc aca ata aaa gaa ctg agg cgg ctt ttc tta gtt		3249

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His	Val	Asn	Ser	Thr	Ile	Lys	Glu	Leu	Arg	Arg	Leu	Phe	Leu	Val	
1070						1075									1080
gat	gat	tta	gtt	gat	tcc	ctg	aag	ttt	gca	gtg	ttg	atg	tgg	gtg	3294
Asp	Asp	Leu	Val	Asp	Ser	Leu	Lys	Phe	Ala	Val	Leu	Met	Trp	Val	
1085						1090									1095
ttt	act	tat	gtt	ggt	gcc	ttg	ttc	aat	ggt	ctg	aca	cta	ctg	att	3339
Phe	Thr	Tyr	Val	Gly	Ala	Leu	Phe	Asn	Gly	Leu	Thr	Leu	Leu	Ile	
1100						1105					1110				
tta	gct	ctg	atc	tca	ctc	ttc	agt	att	cct	gtt	att	tat	gaa	cgg	3384
Leu	Ala	Leu	Ile	Ser	Leu	Phe	Ser	Ile	Pro	Val	Ile	Tyr	Glu	Arg	
1115						1120					1125				
cat	cag	gtg	cag	ata	gat	cat	tat	cta	gga	ctt	gca	aac	aag	agt	3429
His	Gln	Val	Gln	Ile	Asp	His	Tyr	Leu	Gly	Leu	Ala	Asn	Lys	Ser	
1130						1135					1140				
gtt	aag	gat	gcc	atg	gcc	aaa	atc	caa	gca	aaa	atc	cct	gga	ttg	3474
Val	Lys	Asp	Ala	Met	Ala	Lys	Ile	Gln	Ala	Lys	Ile	Pro	Gly	Leu	
1145						1150					1155				
aag	cgc	aaa	gca	gat	tga										3492
Lys	Arg	Lys	Ala	Asp											
1160															

<210> 26

<211> 1163

<212> PRT

<213> Rattus norvegicus

<400> 26

Met	Glu	Asp	Ile	Asp	Gln	Ser	Ser	Leu	Val	Ser	Ser	Ser	Thr	Asp	Ser
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Pro	Pro	Arg	Pro	Pro	Pro	Ala	Phe	Lys	Tyr	Gln	Phe	Val	Thr	Glu	Pro
20							25					30			

Glu	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Asp	Asp	
35					40					45					

Glu	Asp	Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys	Pro	Ala	Ala	Gly
50					55					60					

Leu	Ser	Ala	Ala	Ala	Ala	Val	Pro	Pro	Ala	Ala	Ala	Pro	Leu	Leu	Asp
65						70						75			80

Phe	Ser	Ser	Asp	Ser	Val	Pro	Pro	Ala	Pro	Arg	Gly	Pro	Leu	Pro	Ala
85						90									95

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Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro
100 105 110

Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Val Leu Pro Ser
115 120 125

Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro
130 135 140 145

Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr
145 150 155 160

Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu
165 170 175

Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu
180 185 190

Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly
195 200 205

Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro
210 215 220

Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu
225 230 235 240

Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr
245 250 255

Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe
260 265 270

Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
275 280 285

Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val
290 295 300

Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp
305 310 315 320

Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly
325 330 335

Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn
340 345 350

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Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp
355 360 365

Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
370 375 380

Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp
385 390 395 400

Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp
405 410 415

Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro
420 425 430

Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser
435 440 445

Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His
450 455 460

Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala
465 470 475 480

Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu
485 490 495

Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu
500 505 510

Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
515 520 525

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
530 535 540

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
545 550 555 560

Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
565 570 575

Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
580 585 590

Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val

Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
610 615 620 625 630 635 640
Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
645 650 655
Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
660 665 670
Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro
675 680 685
Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser
690 695 700
Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu
705 710 715 720
Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr
725 730 735
Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser
740 745 750
Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln
755 760 765
Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser
770 775 780
Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu
785 790 795 800
Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn
805 810 815
Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr
820 825 830
Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe
835 840 845

4-32761A_UNZ.ST25.txt

Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
 850 855 860

Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
 865 870 875 880

Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn
 885 890 895

Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn
 900 905 910

Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala
 915 920 925

Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu
 930 935 940

Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp
 945 950 955 960

Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val
 965 970 975

Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe
 980 985 990

Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val
 995 1000 1005

Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile
 1010 1015 1020

Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser
 1025 1030 1035

Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala
 1040 1045 1050

Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly
 1055 1060 1065

His Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val
 1070 1075 1080

Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val
 1085 1090 1095

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Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile
1100 1105 1110

Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg
1115 1120 1125

His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Ser
1130 1135 1140

Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu
1145 1150 1155

Lys Arg Lys Ala Asp
1160

<210> 27

<211> 25

<212> PRT

<213> *Rattus norvegicus*

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> rat PEP4

<400> 27

Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn
1 5 10 15

Ser Thr Ile Lys Glu Leu Arg Arg Leu
20 25

<210> 28

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> PRO/SER rich peptide

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Synthetic peptide

<400> 28

Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro
1 5 10 15

Ser

<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-2F

<220>

<221> primer_bind

<222> (1)..(25)

<223> CA-NA-2F primer

<400> 29

aagcaccatt gaattctgca gttcc

25

<210> 30

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-3R

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<220>
<221> primer_bind
<222> (1)..(28)
<223>

<400> 30
aactgcagta ctgagctcct ccatctgc

28

<210> 31
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> forward 5'
<220>
<221> primer_bind
<222> (1)..(33)
<223> forward primer

<400> 31
gtcgcggatc catggagacc cttttgctc ttc

33

<210> 32
<211> 27
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<220>
<223> reverse 5'
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<222> (1)..(27)

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<223> reverse primer

<400> 32
gttctcgagt tatgaagttt tactcag

27

<210> 33

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> forward 5'-1

<220>

<221> primer_bind

<222> (1)..(29)

<223> primer

<400> 33
gtgcggatcc atggatttga aggagcagc

29

<210> 34

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse 5'-1

<220>

<221> primer_bind

<222> (1)..(28)

<223> primer

<400> 34
gtttctcgag tgaagttta ttcagctc

28

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<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' primer
<220>
<221> primer_bind
<222> (1)..(20)
<223> primer

<400> 35
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<210> 36
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' primer 2
<220>
<221> primer_bind
<222> (1)..(22)
<223> primer

<400> 36
aatgatgggc aaagctgtgc tg
<210> 37
<211> 24
<212> DNA

20

22

<213> Artificial Sequence

<220>

<223> 3' primer

<220>

<221> primer_bind

<222> (1)..(24)

<223> primer

<400> 37
ggtacaaaga ttgcttatga aaca

24

<210> 38

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' primer 2

<220>

<221> primer_bind

<222> (1)..(22)

<223> primer

<400> 38
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22

<210> 39

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> 5'-VL leader

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<220>
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<222> (1)..(28)
<223> primer

<400> 39
aatatgagtc ctgccagtt cctgttcc

28

<210> 40
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> 3'-ck
<220>
<221> primer_bind
<222> (1)..(32)
<223> primer

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32

<210> 41
<211> 31
<212> DNA
<213> Artificial sequence

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<223> 5'-vh leader
<220>
<221> primer_bind
<222> (1)..(31)

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<223> primer

<400> 41
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<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 3'-CH hinge

<220>

<221> primer_bind

<222> (1)..(24)

<223> primer

<400> 42
aattggcaa cgttgcaggt gacg 24

<210> 43

<211> 663

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1)..(663)

<223> DNA variable part of heavy chain 11c7

<400> 43
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aagcttctcg agtctggagg tggcctggtg cagcctggag gatccctgaa actctcctgt 120
gtagtctcag gattcgattt tagaagaaat tggatgagtt gggtccggca ggctcctgg 180

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aaaggctag aatggattgg agaaattaat ccagatagca gtaagataaa ctatacgca	240
tctctaaagg ataaattcat catctccaga gacaatgcc aaaaaaaaaaaaaa	300
gtgagcacag tgagatctga ggacacagcc ctttattact gtgtgagacc ggtctggatg	360
tatgctatgg actactgggg tcaaggaacc tcagtcaccg tctcctcagc caaaacgaca	420
cccccatctg tctatccact ggccctgga tctgctgccc aaactaactc catggtgacc	480
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tccctgtcca gcggtgtgca caccccca gctgtcctgc agtctgaccc ctacactctg	600
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gcc	663
<210> 44	
<211> 717	
<212> DNA	
<213> <i>Mus musculus</i>	
<220>	
<221> misc_binding	
<222> (1)..(717)	
<223> variable part of light chain of 11c7	
<400> 44	
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gttctgttga cccagactcc tctcaacttg tcgataacca ttggacaacc agcctccatc	120
tcttgcaagt caagtcagag cctcttgcat agtgtatggaa agacatattt gaattggttg	180
ttacagaggc caggccagtc tccaaagcgc ctaatctatc tgggtctaa actggactct	240
ggagtcctg acaggttac tggcagtggaa tcagggacgg atttcacact gaaaatcagc	300
agagtggagg ctgaggattt gggactttat tattgctggc aaggtacaca ttttcctcag	360
acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc	420
atcttccac catccagtga gcagttaca tctggaggtg cctcagtcgt gtgcttcttg	480
aacaacttct accccaaaga catcaatgtc aagtggaaaga ttgatggcag tgaacgacaa	540
aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc	600
agcaccctca cgttgaccaa ggacgagttt gAACGACATAACAGCTATACTCTGAGGCC	660
actcacaaga catcaacttc acccattgtc aagagcttca acaggggaga gtgttag	717

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